

## WHAT IS CLAIMED IS:

1	1.	A set of nucleic acids comprising:		
2		a first pair of primers, each containing an oligo-nucleotide selected from the		
3		hemagglutinin-neuraminidase gene region of human parainfluenza virus 2, and		
4		a second pair of primers, each containing an oligo-nucleotide selected from the		
5		hexon gene region of adenovirus,		
6		wherein each oligo-nucleotide has 14-40 nucleotides in length.		
7				
1	2.	The set of nucleic acids of claim 1, further comprising:		
2		a third pair of primers, each containing an oligo-nucleotide specific for human		
3		parainfluenza virus 1;		
3.1.0105888355 0.1010 1010		a fourth pair of primers, each containing an oligo-nucleotide specific for human		
5		parainfluenza virus 3;		
61		a fifth pair of primers, each containing an oligo-nucleotide specific for respiratory		
بي آين		syncytial virus;		
8		a sixth pair of primers, each containing an oligo-nucleotide specific for influenza		
9		virus A; or		
10		a seventh pair of primers, each containing an oligo-nucleotide specific for		
1点		influenza virus B;		
12		or a combination thereof.		
13				
1	3.	The set of nucleic acids of claim 2, wherein		
2		the oligo-nucleotides in the third pair of primers are selected from the		
3		hemagglutinin-neuraminidase gene region of human parainfluenza virus 1,		
4		the oligo-nucleotides in the fourth pair of primers are selected from the		
5		hemagglutinin-neuraminidase gene region of human parainfluenza virus 3,		
6		the oligo-nucleotides in the fifth pair of primers are selected from the non-		
7		structural protein 2 gene region of respiratory syncytial virus,		
8		the oligo-nucleotides in the sixth pair of primers are selected from the non-		
9		structural protein gene region of influenza virus A, and		



10		the oligo-nucleotides in the seventh pair of primers are selected from the
11		hemagglutinin-neuraminidase gene region of influenza virus B.
12		
1	4.	The set of nucleic acids of claim 1, wherein
2		the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:5
3		and 7, or SEQ ID NOs:6 and 7; and
4		the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID
5		NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27.
6		
1	5.	The set of nucleic acids of claim 4, further comprising:
2		a third pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:1
3;=≟		and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;
		a fourth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:8
# 1		and 10, SEQ ID NOs:8 and 11, or SEQ IN NOs:9 and 11;
<b>6</b> .		a fifth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:12
W To		and 14, or SEQ ID NOs:13 and 15;
8		a sixth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:
<b>9</b> ≟		16 and 18, or SEQ ID NOs:17 and 19; or
10 <u> </u>		a seventh pair of primers containing, respectively, oligo-nucleotides SEQ ID
11		NO:20 and 22, or SEQ ID NOs:21 and 23,
12 12		or a combination thereof.
13		
1	6.	A set of nucleic acids comprising:
2		a first nucleic acid obtained from amplification of a respiratory syncytial virus
3		nucleic acid template with a first pair of primers, each containing an oligo-nucleotide
4		selected from the non-structural protein 2 gene region;
5		a second nucleic acid obtained from amplification of an influenza virus A nucleic
6		acid template with a second pair of primers, each containing an oligo-nucleotide selected
7		from the non-structural protein gene region; or

	-
4	
-	

a third nucleic acid obtained from amplification of an influenza virus B nucleic
acid template with a third pair of primers, each containing an oligo-nucleotide selected
from the hemagglutinin-neuraminidase gene region,
or a combination thereof,

wherein each oligo-nucleotide has 14-40 nucleotides in length.

7. The set of nucleic acids of claim 6, wherein

the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:12 and 14, or SEQ ID NOs:13 and 15;

the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID NOs: 16 and 18, or SEQ ID NOs:17 and 19; and

the oligo-nucleotides in the third pair of primers are, respectively, SEQ ID NOs:20 and 22, or SEQ ID NOs:21 and 23.

8. The set of nucleic acids of claim 7, further comprising:

a fourth nucleic acid obtained from amplification of a human parainfluenza virus 1 nucleic acid template with a fourth pair of primers, said fourth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:1 and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;

a fifth nucleic acid obtained from amplification of a human parainfluenza virus 2 nucleic acid template with a fifth pair of primers, said fifth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:5 and 7, or SEQ ID NOs:6 and 7;

a sixth nucleic acid obtained from amplification of a human parainfluenza virus 3 nucleic acid template with a sixth pair of primers, said sixth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:8 and 10, SEQ ID NOs:8 and 11, or SEQ IN NOs:9 and 11; or

a seventh nucleic acid obtained from amplification of an adenovirus nucleic acid template with a seventh pair of primers, said seventh pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27;

or a combination thereof.



1	8

1

- 9. A set of nucleic acids comprising:
- 2
- 3
- 4 5
- 6
- 7
- 8
- 9

- 1
- 2 3

1

- 2 3
- 1
- 4
- 2 3

15.

14.

- a first nucleic acid containing a first oligo-nucleotide selected from the non-
- structural protein 2 gene region of respiratory syncytial virus,
- a second nucleic acid containing a second oligo-nucleotide selected from the nonstructural protein gene region of influenza virus A, or
- a third nucleic acid containing a third oligo-nucleotide selected from the hemagglutinin-neuraminidase gene region of influenza virus B,
  - or a combination thereof,
- wherein each nucleic acid has 20-1,000 nucleotides in length.
- The set of nucleic acids of claim 9, wherein each nucleic acid has 20-500 nucleotides in 10. length.
- The set of nucleic acids of claim 10, wherein each nucleic acid has 20-50 nucleotides in 11. length.
- The set of nucleic acids of claim 9, wherein each oligo-nucleotide is selected from the 12. group consisting of SEQ ID NOs:40-52 and sequences complementary thereto.
- The set of nucleic acids of claim 12, wherein each nucleic acid has 20-500 nucleotides in 13. length.
  - The set of nucleic acids of claim 13, wherein each nucleic acid has 20-50 nucleotides in length.

The set of nucleic acids of claim 12, further comprising a nucleic acid containing an

- oligo-nucleotide selected from the group consisting of SEQ ID NOs:28-39, 53-57, and sequences complementary thereto, wherein each nucleic acid has 20-1,000 nucleotides in
- length.



1	16.	The set of nucleic acids of claim 15, wherein each nucleic acid has 20-500 nucleotides in
2		length.
3		
1	17.	The set of nucleic acids of claim 16, wherein each nucleic acid has 20-50 nucleotides in
2		length.
3		
1	18.	A method of simultaneously detecting viruses which cause respiratory infections
2		comprising:
3		providing a nucleic acid from a sample suspected of containing a virus to be
4		detected;
5		amplifying the nucleic acid with a set of primers specific for a group of target
6		viruses, said set of primers containing a first pair of primers, each having an oligo-
道 겙		nucleotide selected from the hemagglutinin-neuraminidase gene region of human
51607583 55 10 11 12 14 13 14 13 14 15 15 15 15 15 15 15 15 15 15 15 15 15		parainfluenza virus 2, and a second pair of primers, each having an oligo-nucleotide
911		selected from the hexon gene region of adenovirus, each oligo-nucleotide having 14-40
10:		nucleotides in length; and
11		detecting amplification products;
12=		whereby detection of an amplification product specific for a target virus indicates the
수 13 <u>급</u>		presence of the target virus.
14 <sup>7U</sup>		
1	19.	The method of claim 18, wherein, in the amplifying step, said set of primers further
2		containing:
3		a third pair of primers, each including an oligo-nucleotide specific for human
4		parainfluenza virus 1,
5		a fourth pair of primers, each including an oligo-nucleotide specific for human
6		parainfluenza virus 3,
7		a fifth pair of primers, each including an oligo-nucleotide specific for respiratory
8		syncytial virus,

9

10

virus A, or

a sixth pair of primers, each including an oligo-nucleotide specific for influenza



11		a seventh pair of primers, each including an oligo-nucleotide specific for
12		influenza virus B,
13		or a combination thereof.
14		
1	20.	The method of claim 19, wherein
2		the oligo-nucleotides in the third pair of primers are selected from the
3		hemagglutinin-neuraminidase gene region of human parainfluenza virus 1,
4		the oligo-nucleotides in the fourth pair of primers are selected from the
5		hemagglutinin-neuraminidase gene region of human parainfluenza virus 3,
6		the oligo-nucleotides in the fifth pair of primers are selected from the non-
7		structural protein 2 gene region of respiratory syncytial virus,
8		the oligo-nucleotides in the sixth pair of primers are selected from the non-
9		structural protein gene region of influenza virus A, and
₩ 10∭		the oligo-nucleotides in the seventh pair of primers are selected from the
		hemagglutinin-neuraminidase gene region of influenza virus B.
: 1	21.	The method of claim 18, wherein
<u>j -</u> 2-		the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:5
3 <u>F</u>		and 7, or SEQ ID NOs:6 and 7; and
□ 41⊍		the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID
5		NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27.
6		
1	22.	The method of claim 21, wherein said set of primers further containing:
2		a third pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:1
3		and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;
4		a fourth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:8
5		and 10, SEQ ID NOs:8 and 11, or SEQ IN NOs:9 and 11;
6		a fifth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:12
7		and 14, or SEQ ID NOs:13 and 15;
8		a sixth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs: 16
9		and 18, or SEQ ID NOs:17 and 19; or



Oocket No.: 12674-006001

		ey Docket No.: 12674
10	a seventh pair of primers including, res	spectively, oligo-nucleotides SEQ ID
11	NO:20 and 22, or SEQ ID NOs:21 and 23;	
12	or a combination thereof.	

13

1

2

3

4

5

6

7

6

7

8

9

10

11

12

13

14

15

3,

23. The method of claim 18, wherein the detecting step includes hybridizing the amplification product to a set of probes, said set of probes containing:

a first probe having a first nucleic acid selected from the hemagglutininneuraminidase gene region of human parainfluenza virus 2, and

a second probe having a second nucleic acid selected from the hexon gene region of adenovirus,

each probe having 20-2000 nucleotides in length.

- 24. The method of claim 23, wherein each nucleic acid is selected from the group consisting of SEQ ID NOs:34-36 and 53-57.
- 25. The method of claim 19, wherein the detecting step includes hybridizing the amplification product to a set of primers, said set of probes contains:

a first probe having a first nucleic acid selected from the hemagglutininneuraminidase gene region of human parainfluenza virus 2, and

a second probe having a second nucleic acid selected from the hexon gene region of adenovirus;

said set of probes further contains:

a third probe having a third nucleic acid specific for human parainfluenza virus 1, a fourth probe having a fourth nucleic acid specific for human parainfluenza virus

a fifth probe having a fifth nucleic acid specific for respiratory syncytial virus, a sixth probe having a sixth nucleic acid specific for influenza virus A, or a seventh probe having a seventh nucleic acid specific for influenza virus B, or a combination thereof;

each probe having 20-2000 nucleotides in length.



- ey Docket No.: 12674-006001
- The method of claim 25, wherein each probe is selected from the group consisting of 26. 1
- SEQ ID NOs:28-57. 2